



SEQUENCE LISTING

<110> Callen, Walter
Richardson, Toby
Frey, Gerhard
Miller, Carl
Kazaoka, Martin
Short, Jay
Mathur, Eric

<120> ENZYMES HAVING ALPHA AMYLASE ACTIVITY
AND METHODS OF USE THEREOF

<130> 09010-107001

<140> 10/081,739

<141> 2002-02-21

<150> 60/270,495

<151> 2001-02-21

<150> 60/270,496

<151> 2001-02-21

<150> 60/291,122

<151> 2001-05-14

<160> 69

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1311

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated

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gccggaatct	ccgcaatatg	gattcccccg	gcgagcaagg	gcatgggcgg	cgcctattcg	180
atgggctacg	acccctacga	cttctttgac	ctcgggtgagt	acgaccagaa	gggaacggta	240
gagacgcgct	ttggctccaa	gcaggagctc	gtgaacatga	taaacaccgc	ccacgcctat	300
ggcatgaagg	taatagccga	tatagtcata	aaccaccgcg	ccggcggtga	cctggagtgg	360
aacccttcg	tgaacgacta	tacctggacc	gacttctcaa	aggtcgcgct	gggtaaatac	420
acggccaact	acctcgactt	ccaccogaac	gagctccatg	cgggcgattc	cggaacattt	480
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caggagagct	acgcggcata	tctcaggagc	atcggcatcg	atgcctggcg	cttcgactac	600
gtcaagggct	atgctccctg	ggtcgtcaag	gactggctga	actggtgggg	aggctgggag	660
gttgagaggt	actgggacac	caacgtcgac	gctgttctca	actgggcata	ctcgagcggt	720
gccaaaggct	ttgacttcgc	cctctactac	aagatggatg	aggcctttga	caacaaaaac	780
attccagcgc	tcgtctctgc	ccttcagaac	ggccagactg	ttgtctcccg	cgaccggttc	840
aaggccgtaa	cctttgtagc	aaaccacgac	accgatataa	tctqqaacaa	qtatccaqcc	900
tacgcgttca	tcctcaccta	cgaggggccag	ccgacaatat	tctaccgcga	ctacgaggag	960

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tggtcaaca aggataagct caagaacctc atctggatac atgagaacct cgccggagga 1020
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gacaagccgg ggcttataac ctacatcaac ctaggctcga gcaaggccgg aaggtgggtt 1140
tatgtgccga agttcgcggg cgcgtgcata caccagatata ctggtaacct cggaggctgg 1200
gtagacaagt acgtctactc aagcggctgg gtctatctcg aagctccagc ttacgacctt 1260
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<210> 2

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically engineered

<400> 2

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
35          40          45
Pro Pro Ala Ser Lys Gly Met Gly Gly Ala Tyr Ser Met Gly Tyr Asp
50          55          60
Pro Tyr Asp Phe Phe Asp Leu Gly Glu Tyr Asp Gln Lys Gly Thr Val
65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Val Asn Met Ile Asn Thr
85          90          95
Ala His Ala Tyr Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His
100         105         110
Arg Ala Gly Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr
115         120         125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
130         135         140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
145         150         155         160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
165         170         175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
180         185         190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val
195         200         205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
210         215         220
Trp Asp Thr Asn Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly
225         230         235         240
Ala Lys Val Phe Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe
245         250         255
Asp Asn Lys Asn Ile Pro Ala Leu Val Ser Ala Leu Gln Asn Gly Gln
260         265         270
Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn
275         280         285
His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile
290         295         300
Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
305         310         315         320
Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Glu Asn

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	325		330		335										
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Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Asp	Lys	Pro	Gly	Leu	Ile	Thr	Tyr
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Ile	Asn	Leu	Gly	Ser	Ser	Lys	Ala	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys
	370		375		380										
Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp
385			390		395					400					
Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro
	405		410		415										
Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr
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Cys	Gly	Val	Gly												
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<210> 3

<211> 1419

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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gatggcacgt	tatggacca	agtggccaat	gaagccaaca	acttatccag	ccttgccatc	180
accgctcttt	ggctgccgcc	cgcttacaaa	ggaacaagcc	gcagcgacgt	agggtacgga	240
gtatacgact	tgtatgacct	cggcgaattc	aatcaaaaag	ggaccgtccg	cacaaaatac	300
ggaacaaaag	ctcaatatct	tcaagccatt	caagccgccc	acgccgtggg	aatgcaagtg	360
tacgccgatg	tcgtgttcga	ccataaaggg	ggcgctgacg	gcacggaatg	ggtggacgcc	420
gtcgaagtca	atccgtccga	cgcgaaccaa	gaaatctcgg	gcacctatca	aatccaagca	480
tggacgaaat	ttgattttcc	cgggcggggc	aacacctact	ccagctttta	gtggcgctgg	540
taccattttg	acggcgttga	ttgggacgaa	agccgaaaat	tgagccgcat	ttacaaattc	600
cgcggcatcg	gcaaagcgtg	ggattgggaa	gtagacacgg	aaaacggaaa	ctatgactac	660
ttaatgtatg	ccgaccttga	tatggatcat	cccgaagtcg	tgaccgagct	gaaaaactgg	720
gggaaatggg	atgtcaacac	aacgaacatt	gatgggttcc	ggcttgatgc	cgtcaagcat	780
attaagttca	gtttttttcc	tgattgggtg	tcgtatgtgc	gttctcagac	tggaagccg	840
ctattttaccg	tcggggaata	ttggagctat	gacatcaaca	agttgcacaa	ttacattacg	900
aaaacagacg	gaacgatgtc	tttgtttgat	gccccgttac	acaacaaatt	ttataccgct	960
tccaaatcag	ggggcgcat	tgatatgcgc	acgttaatga	ccaatactct	catgaaagat	1020
caaccgacat	tgcccgtcac	cttcgttgat	aatcatgaca	ccgaaccggg	ccaagcgctg	1080
cagtcatggg	tcgacccatg	gttcaaaccg	ttggcttacg	cctttattct	aactcggcag	1140
gaaggatacc	cgtgcgtctt	ttatgggtgac	tattatggca	ttccacaata	taacattcct	1200
tcgctgaaaa	gcaaaatcga	tcgcgtcttc	atcgcgcgca	gggattatgc	ttacggaacg	1260
caacatgatt	atcttgatca	ctccgacatc	atcgggtgga	caagggaagg	ggtcactgaa	1320
aaaccaggat	cggggctggc	cgcactgac	accgatgggc	cgggaggaag	caaatggatg	1380
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<210> 4

<211> 1539

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 4

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gaatgggtaca	tgcccaatga	cggccaacat	tggaaagcgt	tgcaaaacga	ctcggcatat	180
ttggctgaac	acggtattac	tgcctgtctg	attcccccg	catataaggg	aacgagccaa	240
gcggatgtgg	gctacgggtg	ttacgacctt	tatgatttag	gggagtttca	tcaaaaaggg	300
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accgaagatg	taaccgcggg	tgaagtcgat	cccgtgacc	gcaaccgcgt	aatttcagga	480
gaacaccgaa	ttaaagcctg	gacacatttt	cattttccgg	ggcgcggcag	cacatacagc	540
gatttttaaat	ggcattggta	ccattttgac	ggaaccgatt	gggacgagtc	ccgaaagctg	600
aaccgcatct	ataagtttca	aggaaaggct	tgggattggg	aagtttccaa	tgaaaacggc	660
aactatgatt	atttgatgta	tgccgacatc	gattatgacc	atcctgatgt	cgcagcagaa	720
attaagagat	ggggcacttg	gtatgccaat	gaactgcaat	tggacggttt	ccgtcttgat	780
gctgtcaaac	acattaaatt	ttcttttttg	cgggattggg	ttaatcatgt	cagggaaaaa	840
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aactatttga	acaaaacaaa	ttttaatcat	tcagtgtttg	acgtgccgct	tcattatcag	960
ttccatgctg	catcgacaca	gggaggcggc	tatgatatga	ggaaattgct	gaacggtacg	1020
gtcgtttcca	agcatccggt	gaaagcgggt	acatttgcg	ataaccatga	tacacagccg	1080
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gactcccagc	gcgaaattcc	tgccttgaaa	cacaaaattg	aaccgatctt	aaaagcgaga	1260
aaacagtatg	cgtacggagc	acagcatgat	tatttcgacc	accatgacat	tgtcggctgg	1320
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cccgtgggg	caaagcgaat	gtatgtcggc	cggcaaaacg	ccggtgagac	atggcatgac	1440
attaccggaa	accgttcgga	gccggttgct	atcaattcgg	aaggctgggg	agagtttcac	1500
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<210> 5

<211> 1395

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

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atgcaggcct	tctactggga	tgttcccggg	gggggaatct	ggtgggacac	cataagacag	180
aaaatcccgg	agtgggtacg	cgctggaatc	tcggcgatat	ggattcctcc	agctagcaaa	240
gggatgggcg	gtgggtattc	catgggctac	gatccctacg	atttctttga	cctcggcgag	300
tactatcaga	agggaacagt	tgagacgcgc	ttcggtcaa	aggaggaact	ggtgaacatg	360
ataaacaccg	cacactccta	tggcataaag	gtgatagcgg	acatagtcac	aaaccaccgc	420
gccggtggag	accttgagtg	gaaccccttt	gtaaacaact	atacttgga	agacttctcc	480
aaggtcgctt	ccggtaaata	cacggccaac	taccttgact	tcaccccaaa	cgaggtcaag	540
tgtctcgatg	agggtacatt	tggtagcttt	ccggacatcg	cccacgagaa	gagctgggat	600
cgtactggc	tctgggcaag	caatgagagc	tacgccgcac	atctccggag	catagggatc	660
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cacgagcacc	ttgccggagg	aagtaccaag	atcctctact	acgataacga	tgagctaata	1140

ttcatgaggg	agggctacgg	gagcaagccg	ggcctcataa	cctacataaa	cctcggaac	1200
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<210> 6
 <211> 1386
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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ggttgaagg	gggtttatgt	gccgaagttc	gcgggcgcgt	gcatccacga	gtatactggt	1260
aacctcggag	gctgggtaga	caagtacgtc	tactcaagcg	gctgggtcta	tctcgaagct	1320
ccagcttacg	accctgccaa	cgggcagtat	ggctactccg	tgtggagcta	ttgcggtggt	1380
gggtga						1386

<210> 7
 <211> 472
 <212> PRT
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

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Gly	Gln	Pro	Ala	Lys	Ala	Ala	Ala	Pro	Phe	Asn	Gly	Thr	Met	Met	Gln
			20					25					30		
Tyr	Phe	Glu	Trp	Tyr	Leu	Pro	Asp	Asp	Gly	Thr	Leu	Trp	Thr	Lys	Val
		35					40					45			
Ala	Asn	Glu	Ala	Asn	Asn	Leu	Ser	Ser	Leu	Gly	Ile	Thr	Ala	Leu	Trp
	50					55					60				

Leu	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Arg	Ser	Asp	Val	Gly	Tyr	Gly	65	70	75	80
Val	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	85	90	95	
Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ala	Gln	Tyr	Leu	Gln	Ala	Ile	Gln	Ala	100	105	110	
Ala	His	Ala	Ala	Gly	Met	Gln	Val	Tyr	Ala	Asp	Val	Val	Phe	Asp	His	115	120	125	
Lys	Gly	Gly	Ala	Asp	Gly	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	130	135	140	
Pro	Ser	Asp	Arg	Asn	Gln	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala	145	150	155	160
Trp	Thr	Lys	Phe	Asp	Phe	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	165	170	175	
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Lys	Leu	Ser	Arg	Ile	Tyr	Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	195	200	205	
Trp	Glu	Val	Asp	Thr	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	210	215	220	
Asp	Leu	Asp	Met	Asp	His	Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Asn	Trp	225	230	235	240
Gly	Lys	Trp	Tyr	Val	Asn	Thr	Thr	Asn	Ile	Asp	Gly	Phe	Arg	Leu	Asp	245	250	255	
Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Phe	Pro	Asp	Trp	Leu	Ser	Tyr	260	265	270	
Val	Arg	Ser	Gln	Thr	Gly	Lys	Pro	Leu	Phe	Thr	Val	Gly	Glu	Tyr	Trp	275	280	285	
Ser	Tyr	Asp	Ile	Asn	Lys	Leu	His	Asn	Tyr	Ile	Thr	Lys	Thr	Asp	Gly	290	295	300	
Thr	Met	Ser	Leu	Phe	Asp	Ala	Pro	Leu	His	Asn	Lys	Phe	Tyr	Thr	Ala	305	310	315	320
Ser	Lys	Ser	Gly	Gly	Ala	Phe	Asp	Met	Arg	Thr	Leu	Met	Thr	Asn	Thr	325	330	335	
Leu	Met	Lys	Asp	Gln	Pro	Thr	Leu	Ala	Val	Thr	Phe	Val	Asp	Asn	His	340	345	350	
Asp	Thr	Glu	Pro	Gly	Gln	Ala	Leu	Gln	Ser	Trp	Val	Asp	Pro	Trp	Phe	355	360	365	
Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Gln	Glu	Gly	Tyr	Pro	370	375	380	
Cys	Val	Phe	Tyr	Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Gln	Tyr	Asn	Ile	Pro	385	390	395	400
Ser	Leu	Lys	Ser	Lys	Ile	Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	405	410	415	
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Trp	Thr	Arg	Glu	Gly	Val	Thr	Glu	Lys	Pro	Gly	Ser	Gly	Leu	Ala	Ala	435	440	445	
Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ser	Lys	Trp	Met	Tyr	Cys	Trp	Gln	450	455	460	
Thr	Thr	Arg	Trp	Lys	Ser	Val	Leu									465	470		

<210> 8

<211> 512

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 8

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			20					25					30		
Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Met	Pro	Asn	Asp	Gly
		35					40					45			
Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ser	Ala	Tyr	Leu	Ala	Glu	His
	50					55					60				
Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Gln
65					70					75					80
Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe
			85					90					95		
His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	Leu
			100					105					110		
Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr	Gly
		115					120					125			
Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp	Val
	130					135					140				
Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	Gly
145					150					155					160
Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	Gly
			165					170					175		
Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	Thr
		180					185					190			
Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	Gly
	195					200						205			
Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr
	210					215					220				
Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	Glu
225					230					235					240
Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	Gly
			245						250					255	
Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp
		260					265					270			
Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val
		275				280						285			
Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	Asn
	290					295					300				
Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	Gln
305					310					315					320
Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	Leu
			325						330				335		
Leu	Asn	Gly	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr	Phe
		340					345					350			
Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val
	355					360						365			
Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu
	370					375					380				
Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly
385					390					395					400
Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	Ile
			405						410					415	

Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
 420 425 430
 Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
 435 440 445
 Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
 450 455 460
 Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
 465 470 475 480
 Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly Trp
 485 490 495
 Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln Arg
 500 505 510

<210> 9

<211> 464

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

Val Val His Met Lys Leu Lys Tyr Leu Ala Leu Val Leu Leu Ala Val
 1 5 10 15
 Ala Ser Ile Gly Leu Leu Ser Thr Pro Val Gly Ala Ala Lys Tyr Ser
 20 25 30
 Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe Tyr Trp Asp Val
 35 40 45
 Pro Gly Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln Lys Ile Pro Glu
 50 55 60
 Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser Lys
 65 70 75 80
 Gly Met Gly Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Phe Phe
 85 90 95
 Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe Gly
 100 105 110
 Ser Lys Glu Glu Leu Val Asn Met Ile Asn Thr Ala His Ser Tyr Gly
 115 120 125
 Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly Asp
 130 135 140
 Leu Glu Trp Asn Pro Phe Val Asn Asn Tyr Thr Trp Thr Asp Phe Ser
 145 150 155 160
 Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His Pro
 165 170 175
 Asn Glu Val Lys Cys Cys Asp Glu Gly Thr Phe Gly Asp Phe Pro Asp
 180 185 190
 Ile Ala His Glu Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser Asn
 195 200 205
 Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp Arg
 210 215 220
 Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Asn Asp Trp Leu
 225 230 235 240
 Ser Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val
 245 250 255
 Asp Ala Leu Leu Asn Trp Ala Tyr Asp Ser Gly Ala Lys Val Phe Asp
 260 265 270
 Phe Pro Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Thr Asn Ile

275	280	285
Pro Ala Leu Val Tyr Ala	Leu Gln Asn Gly Gly Thr	Val Val Ser Arg
290	295	300
Asp Pro Phe Lys Ala Val	Thr Phe Val Ala Asn His	Asp Thr Asp Ile
305	310	315
Ile Trp Asn Lys Tyr Pro	Ala Tyr Ala Phe Ile Leu	Thr Tyr Glu Gly
325	330	335
Gln Pro Val Ile Phe Tyr	Arg Asp Tyr Glu Glu Trp	Leu Asn Lys Asp
340	345	350
Lys Leu Asn Asn Leu Ile	Trp Ile His Glu His Leu	Ala Gly Gly Ser
355	360	365
Thr Lys Ile Leu Tyr Tyr	Asp Asn Asp Glu Leu Ile	Phe Met Arg Glu
370	375	380
Gly Tyr Gly Ser Lys Pro	Gly Leu Ile Thr Tyr Ile	Asn Leu Gly Asn
385	390	395
Asp Trp Ala Glu Arg Trp	Val Asn Val Gly Ser Lys	Phe Ala Gly Tyr
405	410	415
Thr Ile His Glu Tyr Thr	Gly Asn Leu Gly Gly Trp	Val Asp Arg Trp
420	425	430
Val Gln Tyr Asp Gly Trp	Val Lys Leu Thr Ala Pro	Pro His Asp Pro
435	440	445
Ala Asn Gly Tyr Tyr Gly	Tyr Ser Val Trp Ser Tyr	Ala Gly Val Gly
450	455	460

<210> 10

<211> 461

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 10

Met Lys Lys Phe Val Ala	Leu Phe Ile Thr Met	Phe Phe Val Val Ser
1	5	10
Met Ala Val Val Ala Gln	Pro Ala Ser Ala Ala	Lys Tyr Ser Glu Leu
20	25	30
Glu Glu Gly Gly Val Ile	Met Gln Ala Phe Tyr Trp	Asp Val Pro Gly
35	40	45
Gly Gly Ile Trp Trp Asp	Thr Ile Arg Ser Lys Ile	Pro Glu Trp Tyr
50	55	60
Glu Ala Gly Ile Ser Ala	Ile Trp Ile Pro Pro	Ala Ser Lys Gly Met
65	70	75
Ser Gly Gly Tyr Ser Met	Gly Tyr Asp Pro Tyr	Asp Phe Phe Asp Leu
85	90	95
Gly Glu Tyr Asn Gln Lys	Gly Thr Ile Glu Thr Arg	Phe Gly Ser Lys
100	105	110
Gln Glu Leu Ile Asn Met	Ile Asn Thr Ala His	Ala Tyr Gly Ile Lys
115	120	125
Val Ile Ala Asp Ile Val	Ile Asn His Arg Ala	Gly Gly Asp Leu Glu
130	135	140
Trp Asn Pro Phe Val Gly	Asp Tyr Thr Trp Thr	Asp Phe Ser Lys Val
145	150	155
Ala Ser Gly Lys Tyr Thr	Ala Asn Tyr Leu Asp	Phe His Pro Asn Glu
165	170	175
Val Lys Cys Cys Asp Glu	Gly Thr Phe Gly Gly	Phe Pro Asp Ile Ala
180	185	190

His Glu Lys Ser Trp Asp Gln His Trp Leu Trp Ala Ser Asp Glu Ser
 195 200 205
 Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Val Asp Ala Trp Arg Phe Asp
 210 215 220
 Tyr Val Lys Gly Tyr Gly Ala Trp Val Val Lys Asp Trp Leu Asn Trp
 225 230 235 240
 Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn Val Asp Ala
 245 250 255
 Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe Asp Phe Pro
 260 265 270
 Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Lys Asn Ile Pro Ala
 275 280 285
 Leu Val Ser Ala Leu Gln Asn Gly Gln Thr Val Val Ser Arg Asp Pro
 290 295 300
 Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp Ile Ile Trp
 305 310 315 320
 Asn Lys Tyr Leu Ala Tyr Ala Phe Ile Leu Thr Tyr Glu Gly Gln Pro
 325 330 335
 Val Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys Asp Arg Leu
 340 345 350
 Asn Asn Leu Ile Trp Ile His Asp His Leu Ala Gly Gly Ser Thr Ser
 355 360 365
 Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile Phe Val Arg Asn Gly Tyr
 370 375 380
 Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Gly Ser Ser Lys
 385 390 395 400
 Val Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ala Cys Ile His
 405 410 415
 Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Tyr Val Tyr Ser
 420 425 430
 Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala Tyr Asp Pro Ala Asn Gly
 435 440 445
 Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly
 450 455 460

<210> 11
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 gaacactagt aggaggtaac ttatggcaaa gtattccgag ctcgaag

47

<210> 12
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
 gaacggtctc attccgccag ccagcaaggg gatgagcgg

39

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gaaccgtctc aaaacacggc ccatgcctac ggc 33

<210> 14
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
gaacgtctca cctcgacttc caccccaacg aggtcaag 38

<210> 15
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacgtctca ggcgctttga ctacgtgaag ggc 33

<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gaacgggtctc aacaagatgg atgaggcctt tg 32

<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gaaccgtctc acgatataat ctggaacaag taccttgc 38

<210> 18
<211> 35

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 18
 gaaccgtctc agaagcacga gcatagttta ctacg 35

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 gaaccgtctc aaaggtgggt ttatgtgccg 30

<210> 20
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 20
 gaacgtctca ggaatccaaa tggcggatat tcccgc 36

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 21
 gaacggtctc agtttatcat attgatgagc tcc 33

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 22
 gaaccgtctc agaggtagtt ggcagtatat ttg 33

<210> 23
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 23
 gaacgtctca cgccaggcat caacgccgat g 31

<210> 24
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 24
 gaacgtctca ttgtagtaga gcggaagtc 30

<210> 25
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 25
 gaacggtctc aatcggtgct gtggtttgct ac 32

<210> 26
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 26
 gaaccgtctc acttcacct gcgaggtggt c 31

<210> 27
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 27
 gaaccgtctc accttccaac cttgctcgag c 31

<210> 28
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 28

tcgagactga ctctcaccca acaccgcaat agc

33

<210> 29

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 29

gaacactagt aggaggtaac ttatggccaa gtacctggag ctcgaagagg

50

<210> 30

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 30

gaacggtctc attcccccg c gagcaaggg c

31

<210> 31

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 31

gaaccgtctc aaaacaccgc ccacgcctac gg

32

<210> 32

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 32

gaacgtctca cctcgacttc caccccaac

29

<210> 33

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 33
 gaacgtctca ggcgcttcga ctacgtcaag g 31

 <210> 34
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 34
 gaacggtctc aacaagatgg acgcggcctt tgac 34

 <210> 35
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 35
 gaaccgtctc acgatataat ttggaacaag taccc 35

 <210> 36
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 36
 gaaccgtctc agaagcaccg acatagtcta c 31

 <210> 37
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 37
 gaaccgtctc aaaggtgggt ctacgttcgg 30

 <210> 38
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 38
 gaacgtctca ggaatccata ttgcggagat tccggc 36

<210> 39
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 39
 gaacggtctc agtttatcat gttcacgagc tc 32

<210> 40
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 40
 gaaccgtctc agaggtagtt ggccgtgtac ttg 33

<210> 41
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 41
 gaacgtctca gccatgcgtc aacgccgatg 30

<210> 42
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 42
 gaacgtctca ttgtagtaga gcggaagtc g 31

<210> 43
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 43
 gaacggtctc aatcggtgtc gtggtttgca acg 33

<210> 44

<211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 44
 gaaccgtctc acttccaccg gcgaggtggt cgtg

34

<210> 45
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 45
 gaaccgtctc accttccggc cttgctcgag cc

32

<210> 46
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 46
 tcgagactga ctctcagccc accccgcagt agctc

35

<210> 47
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 47
 gaacactagt aggaggtaac ttatggccaa gtactccgag ctggaagagg

50

<210> 48
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 48
 gaacgggtctc attcctcccg cgagcaaggg

30

<210> 49
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 49

gaaccgtctc aaaacaccgc ccacgcctat g

31

<210> 50

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 50

gaacgtctca cctcgacttc caccgaacg agc

33

<210> 51

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 51

gaacgtctca ggcgcttcga ctacgtcaag g

31

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 52

gaacggtctc aacaagatgg acgaggcctt cg

32

<210> 53

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 53

gaaccgtctc acgatataat ctggaacaag

30

<210> 54

<211> 35

<212> DNA

<213> Artificial Sequence

<220>
<223> Primer

<400> 54
gaaccgtctc agaagcactg acatcgttta ctacg 35

<210> 55
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 55
gaaccgtctc aaaggtgggt ttacgttccg 30

<210> 56
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 56
gaacgtctca ggaatccata tcgccgaaat 30

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 57
gaacggtctc agtttatcat gtttatgagc 30

<210> 58
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 58
gaaccgtctc agaggtagtt ggccgtgtat ttac 34

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 59
gaacgtctca cgccaggcat cgatgccgat 30

<210> 60
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 60
gaacgtctca ttgtagtaga gggcgaagtc aaag 34

<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 61
gaacggtctc aatcggtatc gtggttggct acaaac 36

<210> 62
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 62
gaaccgtctc acttctctcg gcgaggttgt catg 34

<210> 63
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 63
gaaccgtctc accttccggc ttgcttgag gc 32

<210> 64
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 64

36

<213> Artificial Sequence

<223> Primer

38

<213> Unknown

<223> Obtained from an environmental sample

atggctctgg	aagagggcgg	gctcataatg	caggccttct	actgggacgt	ccccatggga	60
ggaatctggt	gggacacgat	agcccagaag	atacccgact	gggcaagcgc	cgggatttcg	120
gcgatatgga	tccctcccg	gagcaagggt	atgagcggcg	gctattcgat	gggctacgac	180
ccctacgatt	at ttgtacct	cggtgagtac	taccagaagg	gaacggtgga	aacgaggttc	240
ggctcaaagc	aggagctcat	aaacatgata	aacaccgcc	acgcctatgg	catgaaggta	300
atagccgata	tagtcatcaa	ccaccgcgcc	ggcggtgacc	tggagtggaa	ccccttcgtg	360
aacgactata	cctggaccga	cttctcaaag	gtcgcgtcgg	gtaaatcac	ggccaactac	420
ctcgacttcc	acccgaacga	gctccatg	ggcgattccg	gaacatttgg	aggctatccc	480
gacatatgcc	acgacaagag	ctgggaccag	tactggctct	gggccagcca	ggagagctac	540
gcgcgatatc	tcaggagcat	cggcatcgat	gcctggcgct	tcgactacgt	caagggctat	600
gctccctggg	tcgtcaagga	ctggctgaac	tgggtgggag	gctgggcggg	tggagagtac	660
tgggacacca	acgtcgacgc	tgttctcaac	tgggcatact	cgagcgggtg	caaggtcttt	720
gacttcgccc	tctactacaa	gatggacgag	gccttcgata	acaacaacat	tccgcgctg	780
gtggacgccc	tcagatacgg	tcagacagtg	gtcagccgcg	acccgttcaa	ggctgtgacg	840
tttgtagcca	accacgatac	cgacataatc	tggaacaagt	atccagccta	cgcgttcac	900
ctcacctacg	agggccagcc	gacaatatc	taccgcgact	acgaggagtg	gctcaacaag	960
gataagctca	agaacctcat	ctggatacat	gacaacctcg	cgggagggag	cactgacatc	1020
gtttactacg	acaacgacga	gctgatattc	gtgagaaacg	gctacggaag	caagccggga	1080
ctgataacat	acatcaacct	cgctcaagc	aaagccggaa	ggtgggttta	cgttcggaag	1140
ttcgcaggct	cgtgcataca	cgagtaacc	ggcaattctg	gcggctgggt	ggacaagtgg	1200
gtggactcaa	gcggtctggg	ctacctcgag	gctcctgcc	acgaccggc	caacggccag	1260
tacgqctact	ccgtctqaaq	ctactcqggt	qttgggtga			1299

<213> Unknown

<223> Obtained from an environmental sample

Met Ala Leu Glu Glu Gly Gly Leu Ile Met Gln Ala Phe Tyr Trp Asp
1 5 10 15
Val Pro Met Gly Gly Ile Trp Trp Asp Thr Ile Ala Gln Lys Ile Pro

20	25	30
Asp Trp Ala Ser Ala Gly Ile Ser Ala Ile Trp Ile Pro Pro Ala Ser		
35	40	45
Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro Tyr Asp Tyr		
50	55	60
Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu Thr Arg Phe		
65	70	75
Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala His Ala Tyr		
85	90	95
Gly Met Lys Val Ile Ala Asp Ile Val Ile Asn His Arg Ala Gly Gly		
100	105	110
Asp Leu Glu Trp Asn Pro Phe Val Asn Asp Tyr Thr Trp Thr Asp Phe		
115	120	125
Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu Asp Phe His		
130	135	140
Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly Gly Tyr Pro		
145	150	155
Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu Trp Ala Ser		
165	170	175
Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile Asp Ala Trp		
180	185	190
Arg Phe Asp Tyr Val Lys Gly Tyr Ala Pro Trp Val Val Lys Asp Trp		
195	200	205
Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp Asp Thr Asn		
210	215	220
Val Asp Ala Val Leu Asn Trp Ala Tyr Ser Ser Gly Ala Lys Val Phe		
225	230	235
Asp Phe Ala Leu Tyr Tyr Lys Met Asp Glu Ala Phe Asp Asn Asn Asn		
245	250	255
Ile Pro Ala Leu Val Asp Ala Leu Arg Tyr Gly Gln Thr Val Val Ser		
260	265	270
Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His Asp Thr Asp		
275	280	285
Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu Thr Tyr Glu		
290	295	300
Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp Leu Asn Lys		
305	310	315
Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu Ala Gly Gly		
325	330	335
Ser Thr Asp Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe Val Arg		
340	345	350
Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile Asn Leu Ala		
355	360	365
Ser Ser Lys Ala Gly Arg Trp Val Tyr Val Pro Lys Phe Ala Gly Ser		
370	375	380
Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val Asp Lys Trp		
385	390	395
Val Asp Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala His Asp Pro		
405	410	415
Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys Gly Val Gly		
420	425	430

<210> 68

<211> 1386

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 68

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ccggagtggg	acgatgccgg	aatctccgca	atatggattc	ccccggcgag	caagggcatg	240
ggcggcgcc	attcgatggg	ctacgacccc	tacgacttct	ttgacctcgg	tgagtacgac	300
cagaagggaa	cggtagagac	gcgctttggc	tccaagcagg	agctcgtgaa	catgataaac	360
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aacaagtacc	cggcctacgc	cttcactctc	acctacgagg	gccagccgac	gatattctac	1020
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cacctcgccg	gtggaagcac	cgacatagtc	tactacgata	acgatgaact	catcttcgtc	1140
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<210> 69

<211> 461

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 69

Met	Lys	Pro	Ala	Lys	Leu	Leu	Val	Phe	Val	Leu	Val	Val	Ser	Ile	Leu
1				5				10					15		
Ala	Gly	Leu	Tyr	Ala	Gln	Pro	Ala	Gly	Ala	Ala	Lys	Tyr	Leu	Glu	Leu
		20						25					30		
Glu	Glu	Gly	Gly	Val	Ile	Met	Gln	Ala	Phe	Tyr	Trp	Asp	Val	Pro	Ser
		35					40					45			
Gly	Gly	Ile	Trp	Trp	Asp	Thr	Ile	Arg	Gln	Lys	Ile	Pro	Glu	Trp	Tyr
	50					55					60				
Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Ser	Lys	Gly	Met
65					70					75				80	
Gly	Gly	Ala	Tyr	Ser	Met	Gly	Tyr	Asp	Pro	Tyr	Asp	Phe	Phe	Asp	Leu
				85					90					95	
Gly	Glu	Tyr	Asp	Gln	Lys	Gly	Thr	Val	Glu	Thr	Arg	Phe	Gly	Ser	Lys
			100					105					110		
Gln	Glu	Leu	Val	Asn	Met	Ile	Asn	Thr	Ala	His	Ala	Tyr	Gly	Ile	Lys
		115					120						125		
Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His	Arg	Ala	Gly	Gly	Asp	Leu	Glu
	130						135				140				
Trp	Asn	Pro	Phe	Val	Asn	Asp	Tyr	Thr	Trp	Thr	Asp	Phe	Ser	Lys	Val

145		150		155		160
Ala Ser Gly Lys Tyr	Thr Ala Asn Tyr	Leu Asp Phe His Pro Asn Glu				
	165	170	175			
Val Lys Cys Cys Asp	Glu Gly Thr Phe Gly Gly Phe Pro Asp Ile Ala					
	180	185	190			
His Glu Lys Ser Trp Asp	Gln Tyr Trp Leu Trp Ala Ser Asn Glu Ser					
	195	200	205			
Tyr Ala Ala Tyr Leu Arg Ser	Ile Gly Val Asp Ala Trp Arg Phe Asp					
	210	215	220			
Tyr Val Lys Gly Tyr Gly Ala Trp	Val Val Lys Asp Trp Leu Asp Trp					
225	230	235	240			
Trp Gly Gly Trp Ala Val Gly Glu Tyr	Trp Asp Thr Asn Val Asp Ala					
	245	250	255			
Leu Leu Asn Trp Ala Tyr Ser Ser	Asp Ala Lys Val Phe Asp Phe Pro					
	260	265	270			
Leu Tyr Tyr Lys Met Asp Ala Ala Phe	Asp Asn Lys Asn Ile Pro Ala					
	275	280	285			
Leu Val Glu Ala Leu Lys Asn Gly Gly Thr	Val Val Ser Arg Asp Pro					
	290	295	300			
Phe Lys Ala Val Thr Phe Val Ala Asn His	Asp Thr Asp Ile Ile Trp					
305	310	315	320			
Asn Lys Tyr Pro Ala Tyr Ala Phe Ile	Leu Thr Tyr Glu Gly Gln Pro					
	325	330	335			
Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp	Leu Asn Lys Asp Arg Leu					
	340	345	350			
Lys Asn Leu Ile Trp Ile His Asp His	Leu Ala Gly Gly Ser Thr Asp					
	355	360	365			
Ile Val Tyr Tyr Asp Asn Asp Glu Leu Ile Phe	Val Arg Asn Gly Tyr					
	370	375	380			
Gly Asp Lys Pro Gly Leu Ile Thr Tyr Ile	Asn Leu Gly Ser Ser Lys					
385	390	395	400			
Ala Gly Arg Trp Val Tyr Val Pro Lys Phe	Ala Gly Ala Cys Ile His					
	405	410	415			
Glu Tyr Thr Gly Asn Leu Gly Gly Trp	Val Asp Lys Trp Val Asp Ser					
	420	425	430			
Ser Gly Trp Val Tyr Leu Glu Ala Pro	Ala His Asp Pro Ala Asn Gly					
	435	440	445			
Tyr Tyr Gly Tyr Ser Val Trp Ser Tyr	Cys Gly Val Gly					
450	455	460				